

SEQUENCE LISTING

<110> MARKAU, URSULA

EBENBICHLER, CHRISTINE

ACHHAMMER, GUNTAR

ANKENBAUER, WALTRAUD

<120> MODIFIED DNA-POLYMERASE FROM CARBOXYDOTHENUS HYDROGENOFORMANS AND
ITS USE FOR COUPLED REVERSE TRANSCRIPTION AND POLYMERASE CHAIN REACTION

<130> 1803-332-999

<150> 09/204,208

<151> 1998-12-01

<150> EP 97121151.1

<151> 1997-12-02

<160> 12

<170> PatentIn version 3.0

<210> 1

<211> 18

<212> DNA

<213> Artificial

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<223> Description of artificial sequence: amplification primer

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 Met Glu Lys Leu Ala Glu His Glu Asn Leu Ala Lys Ile Ser Lys Gln
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tta gct aca atc ctg cgg gaa ata ccg tta gaa atc tcc ctg gaa gat 96
 Leu Ala Thr Ile Leu Arg Glu Ile Pro Leu Glu Ile Ser Leu Glu Asp
 20 25 30

tta aaa gtt aaa gaa cct aat tat gaa gaa gtt gct aaa tta ttt ctt 144
 Leu Lys Val Lys Glu Pro Asn Tyr Glu Glu Val Ala Lys Leu Phe Leu

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cac ctt gag ttt aaa agc ttt tta aaa gaa ata gaa cca aaa ata aag 192
 His Leu Glu Phe Lys Ser Phe Leu Lys Glu Ile Glu Pro Lys Ile Lys
 50 55 60

aaa gaa tac cag gaa ggt aaa gat ttg gtg caa gtt gaa act gta gaa 240
 Lys Glu Tyr Gln Glu Gly Lys Asp Leu Val Gln Val Glu Thr Val Glu
 65 70 75 80

acg gaa gga cag att gca gta gtt ttt agt gat gga ttt tat gtt gat 288
 Thr Glu Gly Gln Ile Ala Val Val Phe Ser Asp Gly Phe Tyr Val Asp
 85 90 95

gac ggg gaa aaa aca aag ttt tac tct tta gac cgg ctg aat gaa ata 336
 Asp Gly Glu Lys Thr Lys Phe Tyr Ser Leu Asp Arg Leu Asn Glu Ile
 100 105 110

gag gaa ata ttt agg aat aaa aaa att att acc gac gat gcc aaa gga 384
 Glu Glu Ile Phe Arg Asn Lys Lys Ile Ile Thr Asp Asp Ala Lys Gly
 115 120 125

att tat cat gtc tgt tta gaa aaa ggt ctg act ttt ccc gaa gtt tgt 432
 Ile Tyr His Val Cys Leu Glu Lys Gly Leu Thr Phe Pro Glu Val Cys
 130 135 140

ttt gat gcg cgg att gca gct tat gtt tta aac ccg gcc gac caa aat 480
 Phe Asp Ala Arg Ile Ala Ala Tyr Val Leu Asn Pro Ala Asp Gln Asn
 145 150 155 160

ccc ggc ctc aag ggg ctt tat cta aag tat gac tta ccg gtg tat gaa 528
 Pro Gly Leu Lys Gly Leu Tyr Leu Lys Tyr Asp Leu Pro Val Tyr Glu
 165 170 175

gat gta tct tta aac att aga ggg ttg ttt tat tta aaa aaa gaa atg 576
 Asp Val Ser Leu Asn Ile Arg Gly Leu Phe Tyr Leu Lys Lys Glu Met
 180 185 190

atg aga aaa atc ttt gag cag gag caa gaa agg tta ttt tat gaa ata 624
 Met Arg Lys Ile Phe Glu Gln Glu Gln Arg Leu Phe Tyr Glu Ile
 195 200 205

gaa ctt cct tta act cca gtt ctt gct caa atg gag cat acc ggc att 672
 Glu Leu Pro Leu Thr Pro Val Leu Ala Gln Met Glu His Thr Gly Ile
 210 215 220

cag gtt gac cgg gaa gct tta aaa gag atg tcg tta gag ctg gga gag 720
 Gln Val Asp Arg Glu Ala Leu Lys Glu Met Ser Leu Glu Leu Gly Glu
 225 230 235 240

caa att gaa gag tta atc cgg gaa att tat gtg ctg gcg ggg gaa gag 768
 Gln Ile Glu Glu Leu Ile Arg Glu Ile Tyr Val Leu Ala Gly Glu Glu
 245 250 255

ttt aac tta aac tcg ccc agg cag ctg gga gtt att ctt ttt gaa aaa 816
 Phe Asn Leu Asn Ser Pro Arg Gln Leu Gly Val Ile Leu Phe Glu Lys
 260 265 270

ctt ggg ctg ccg gta att aaa aag acc aaa acg ggc tac tct acc gat 864
 Leu Gly Leu Pro Val Ile Lys Lys Thr Lys Thr Gly Tyr Ser Thr Asp
 275 280 285

gcg gag gtt ttg gaa gag ctc ttg cct ttc cac gaa att atc ggc aaa 912
 Ala Glu Val Leu Glu Glu Leu Leu Pro Phe His Glu Ile Ile Gly Lys

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ata ttg aat tac cgg cag ctt atg aag tta aaa tcc act tat act gac 960
 Ile Leu Asn Tyr Arg Gln Leu Met Lys Leu Lys Ser Thr Tyr Thr Asp 320
 305 310 315

ggc tta atg cct tta ata aat gag cgt acc ggt aaa ctt cac act act 1008
 Gly Leu Met Pro Leu Ile Asn Glu Arg Thr Gly Lys Leu His Thr Thr 335
 325 330

ttt aac cag acc ggt act tta acc gga cgc ctg gcg tct tcg gag ccc 1056
 Phe Asn Gln Thr Gly Thr Leu Thr Gly Arg Leu Ala Ser Ser Glu Pro 350
 340 345

aat ctc caa aat att ccc atc cgg ttg gaa ctc ggt cgg aaa tta cgc 1104
 Asn Leu Gln Asn Ile Pro Ile Arg Leu Glu Leu Gly Arg Lys Leu Arg 365
 355 360

aag atg ttt ata cct tca ccg ggg tat gat tat att gtt tcg gcg gat 1152
 Lys Met Phe Ile Pro Ser Pro Gly Tyr Asp Tyr Ile Val Ser Ala Asp 380
 370 375

tat tcc cag att gaa tta agg ctt ctt gcc cat ttt tcc gaa gag ccc 1200
 Tyr Ser Gln Ile Glu Leu Arg Leu Leu Ala His Phe Ser Glu Glu Pro 400
 385 390 395

aag ctt att gaa gct tac caa aaa ggg gag gat att cac cgg aaa acg 1248
 Lys Leu Ile Glu Ala Tyr Gln Lys Gly Glu Asp Ile His Arg Lys Thr 415
 405 410

gcc tcc gag gtg ttc ggt gta tct ttg gaa gaa gtt act ccc gag atg 1296
 Ala Ser Glu Val Phe Gly Val Ser Leu Glu Glu Val Thr Pro Glu Met 430
 420 425

cgc gct cat gcc aag tcg gtg aac ttc ggc att gtt tat ggc att agt 1344
 Arg Ala His Ala Lys Ser Val Asn Phe Gly Ile Val Tyr Gly Ile Ser 445
 435 440

gat ttt ggt tta ggc aga gac tta aag att ccc cgg gag gtt gcc ggt 1392
 Asp Phe Gly Leu Gly Arg Asp Leu Lys Ile Pro Arg Glu Val Ala Gly 460
 450 455

aag tac att aaa aat tat ttt gcc aac tat ccc aaa gtg cgg gag tat 1440
 Lys Tyr Ile Lys Asn Tyr Phe Ala Asn Tyr Pro Lys Val Arg Glu Tyr 480
 465 470 475

ctc gat gaa ctt gtc cgt acg gca aga gaa aag gga tat gtg acc act 1488
 Leu Asp Glu Leu Val Arg Thr Ala Arg Glu Lys Gly Tyr Val Thr Thr 495
 485 490

tta ttt ggg cga aga cgc tat att cct gag cta tct tca aaa aac cgc 1536
 Leu Phe Gly Arg Arg Arg Tyr Ile Pro Glu Leu Ser Ser Lys Asn Arg 510
 500 505

acg gtt cag ggt ttt ggc gaa agg acg gcc atg aat act ccc ctt cag 1584
 Thr Val Gln Gly Phe Gly Glu Arg Thr Ala Met Asn Thr Pro Leu Gln 525
 515 520

ggc tcg gct gcc gat att att aag ctt gca atg att aat gta gaa aaa 1632
 Gly Ser Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asn Val Glu Lys 540
 530 535

gaa ctt aaa gcc cgt aag ctt aag tcc cgg ctc ctt ctt tcg gtg cac 1680
 Glu Leu Lys Ala Arg Lys Leu Lys Ser Arg Leu Leu Leu Ser Val His

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gat gag tta gtt tta gaa gtg ccg gcg gaa gag ctg gaa gag gta aaa				1728
Asp Glu Leu Val Leu Glu Val Pro Ala Glu Glu Leu Glu Glu Val Lys	565	570	575	
gcg ctg gta aaa ggg gtt atg gag tcg gtg gtt gaa ctg aaa gtg cct				1776
Ala Leu Val Lys Gly Val Met Glu Ser Val Val Glu Leu Lys Val Pro	580	585	590	
tta atc gct gaa gtt ggt gca ggc aaa aac tgg tat gaa gcg aag taa				1824
Leu Ile Ala Glu Val Gly Ala Gly Lys Asn Trp Tyr Glu Ala Lys	595	600	605	
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Met Glu Lys Leu Ala Glu His Glu Asn Leu Ala Lys Ile Ser Lys Gln	1	5	10	15
Leu Ala Thr Ile Leu Arg Glu Ile Pro Leu Glu Ile Ser Leu Glu Asp	20	25	30	
Leu Lys Val Lys Glu Pro Asn Tyr Glu Glu Val Ala Lys Leu Phe Leu	35	40	45	
His Leu Glu Phe Lys Ser Phe Leu Lys Glu Ile Glu Pro Lys Ile Lys	50	55	60	
Lys Glu Tyr Gln Glu Gly Lys Asp Leu Val Gln Val Glu Thr Val Glu	65	70	75	80
Thr Glu Gly Gln Ile Ala Val Val Phe Ser Asp Gly Phe Tyr Val Asp	85	90	95	
Asp Gly Glu Lys Thr Lys Phe Tyr Ser Leu Asp Arg Leu Asn Glu Ile	100	105	110	
Glu Glu Ile Phe Arg Asn Lys Lys Ile Ile Thr Asp Asp Ala Lys Gly	115	120	125	
Ile Tyr His Val Cys Leu Glu Lys Gly Leu Thr Phe Pro Glu Val Cys	130	135	140	
Phe Asp Ala Arg Ile Ala Ala Tyr Val Leu Asn Pro Ala Asp Gln Asn				

145		150		155		160
Pro Gly Leu Lys	Gly Leu Tyr Leu Lys	Tyr Asp Leu Pro Val Tyr Glu				
	165	170			175	
Asp Val Ser Leu Asn Ile Arg Gly Leu Phe Tyr Leu Lys Lys Glu Met						
	180	185			190	
Met Arg Lys Ile Phe Glu Gln Glu Gln Glu Arg Leu Phe Tyr Glu Ile						
	195	200			205	
Glu Leu Pro Leu Thr Pro Val Leu Ala Gln Met Glu His Thr Gly Ile						
	210	215			220	
Gln Val Asp Arg Glu Ala Leu Lys Glu Met Ser Leu Glu Leu Gly Glu						
	225	230			235	240
Gln Ile Glu Glu Leu Ile Arg Glu Ile Tyr Val Leu Ala Gly Glu Glu						
	245			250		255
Phe Asn Leu Asn Ser Pro Arg Gln Leu Gly Val Ile Leu Phe Glu Lys						
	260			265		270
Leu Gly Leu Pro Val Ile Lys Lys Thr Lys Thr Gly Tyr Ser Thr Asp						
	275			280		285
Ala Glu Val Leu Glu Glu Leu Leu Pro Phe His Glu Ile Ile Gly Lys						
	290			295		300
Ile Leu Asn Tyr Arg Gln Leu Met Lys Leu Lys Ser Thr Tyr Thr Asp						
	305			310		315
Gly Leu Met Pro Leu Ile Asn Glu Arg Thr Gly Lys Leu His Thr Thr						
	325			330		335
Phe Asn Gln Thr Gly Thr Leu Thr Gly Arg Leu Ala Ser Ser Glu Pro						
	340			345		350
Asn Leu Gln Asn Ile Pro Ile Arg Leu Glu Leu Gly Arg Lys Leu Arg						
	355			360		365
Lys Met Phe Ile Pro Ser Pro Gly Tyr Asp Tyr Ile Val Ser Ala Asp						
	370			375		380
Tyr Ser Gln Ile Glu Leu Arg Leu Leu Ala His Phe Ser Glu Glu Pro						
	385			390		395
						400
Lys Leu Ile Glu Ala Tyr Gln Lys Gly Glu Asp Ile His Arg Lys Thr						

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Ala Ser Glu Val Phe Gly Val Ser Leu Glu Glu Val Thr Pro Glu Met
420 425 430

Arg Ala His Ala Lys Ser Val Asn Phe Gly Ile Val Tyr Gly Ile Ser
435 440 445

Asp Phe Gly Leu Gly Arg Asp Leu Lys Ile Pro Arg Glu Val Ala Gly
450 455 460

Lys Tyr Ile Lys Asn Tyr Phe Ala Asn Tyr Pro Lys Val Arg Glu Tyr
465 470 475 480

Leu Asp Glu Leu Val Arg Thr Ala Arg Glu Lys Gly Tyr Val Thr Thr
485 490 495

Leu Phe Gly Arg Arg Arg Tyr Ile Pro Glu Leu Ser Ser Lys Asn Arg
500 505 510

Thr Val Gln Gly Phe Gly Glu Arg Thr Ala Met Asn Thr Pro Leu Gln
515 520 525

Gly Ser Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asn Val Glu Lys
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Glu Leu Lys Ala Arg Lys Leu Lys Ser Arg Leu Leu Leu Ser Val His
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Asp Glu Leu Val Leu Glu Val Pro Ala Glu Glu Leu Glu Glu Val Lys
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Ala Leu Val Lys Gly Val Met Glu Ser Val Val Glu Leu Lys Val Pro
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<210> 12

<211> 26

<212> DNA

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<223> Description of artificial sequence: amplification primer

<400> 12
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